



Fig. 2

pCRSP	SCNTATCMTHRLVGLLSRSGSMVRSNLLPTKMGFKVFG-NH2
pCGRP-I	SCNTATCVTHRLAGLLSRSGGMVKSNFVPTDVGSEAF-NH2
hCGRP-I	ACDTATCVTHRLAGLLSRSGGVKNNFVPTNVGSKAF-NH2
hCGRP-II	ACNTATCVTHRLAGLLSRSGGMVKSNFVPTNVGSKAF-NH2
hAmylin	KCNTATCATQRLANFLVHSSNNFGAILSSSTNVGSNTY-NH2
pCT	CSNLSTCVLSAYWRNLNNFHRFSGMGFGPETP-NH2
hAM	YRQSMNMFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY-NH2

Fig. 3

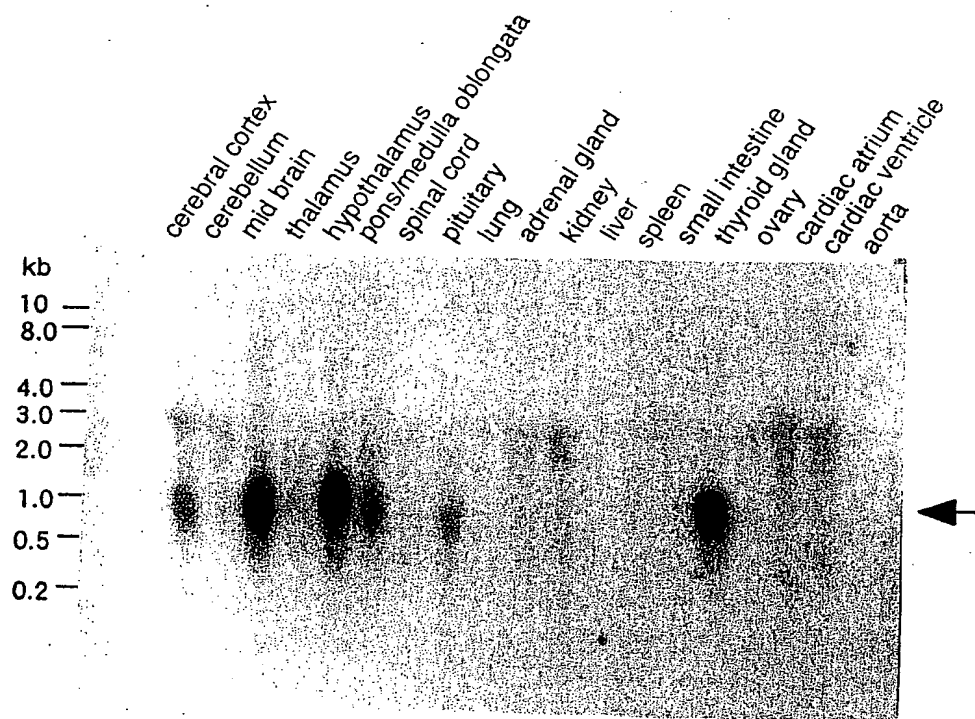


Fig. 4

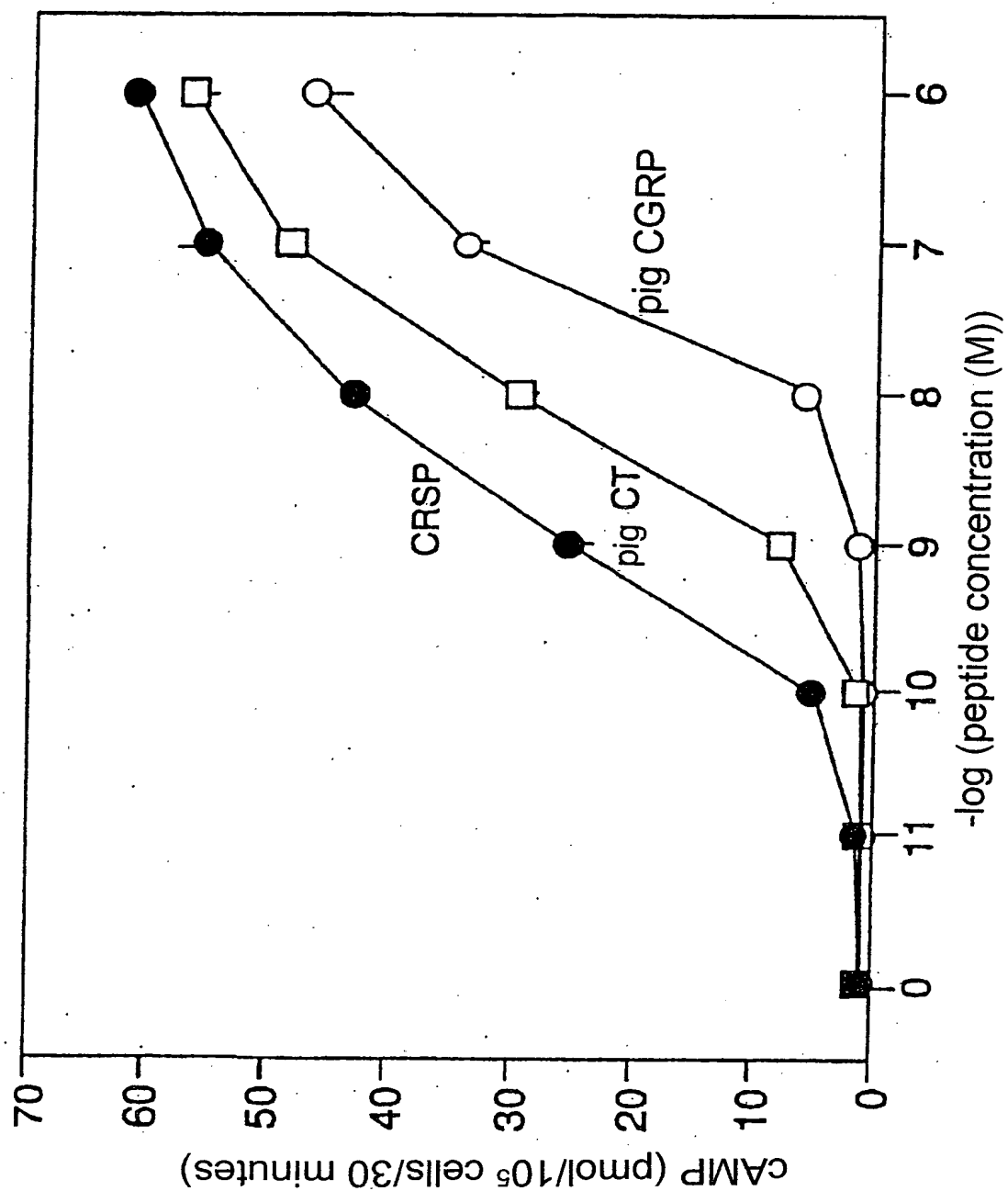


Fig. 5

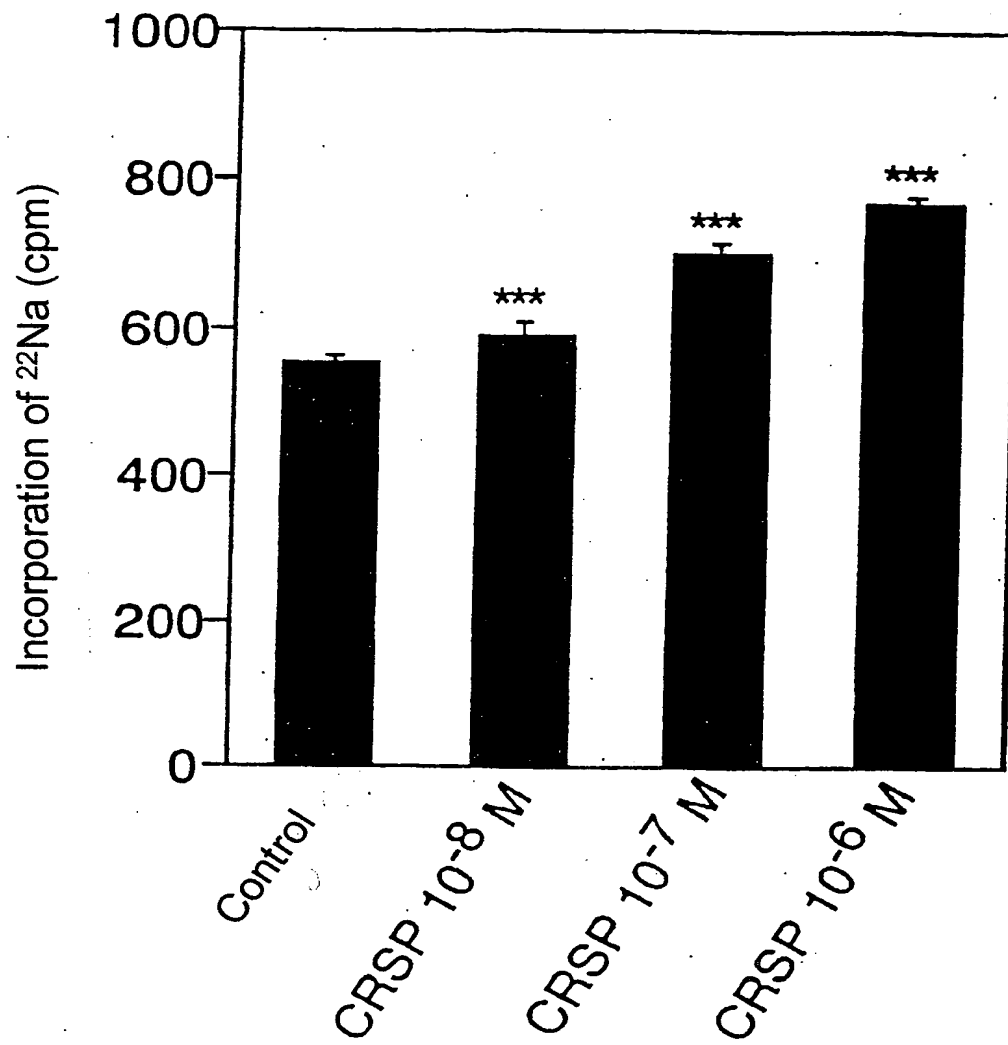


Fig. 6

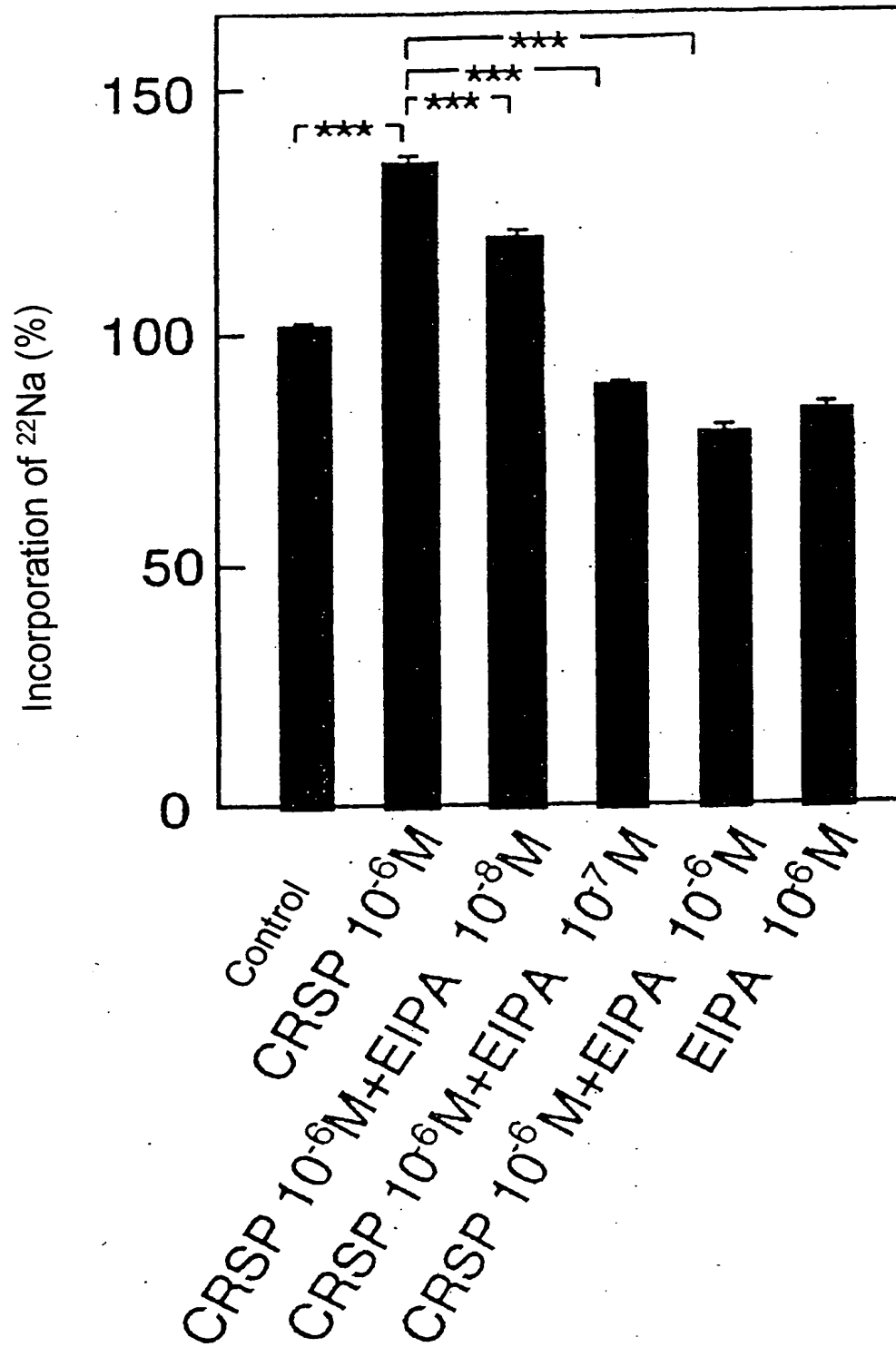


Fig. 7

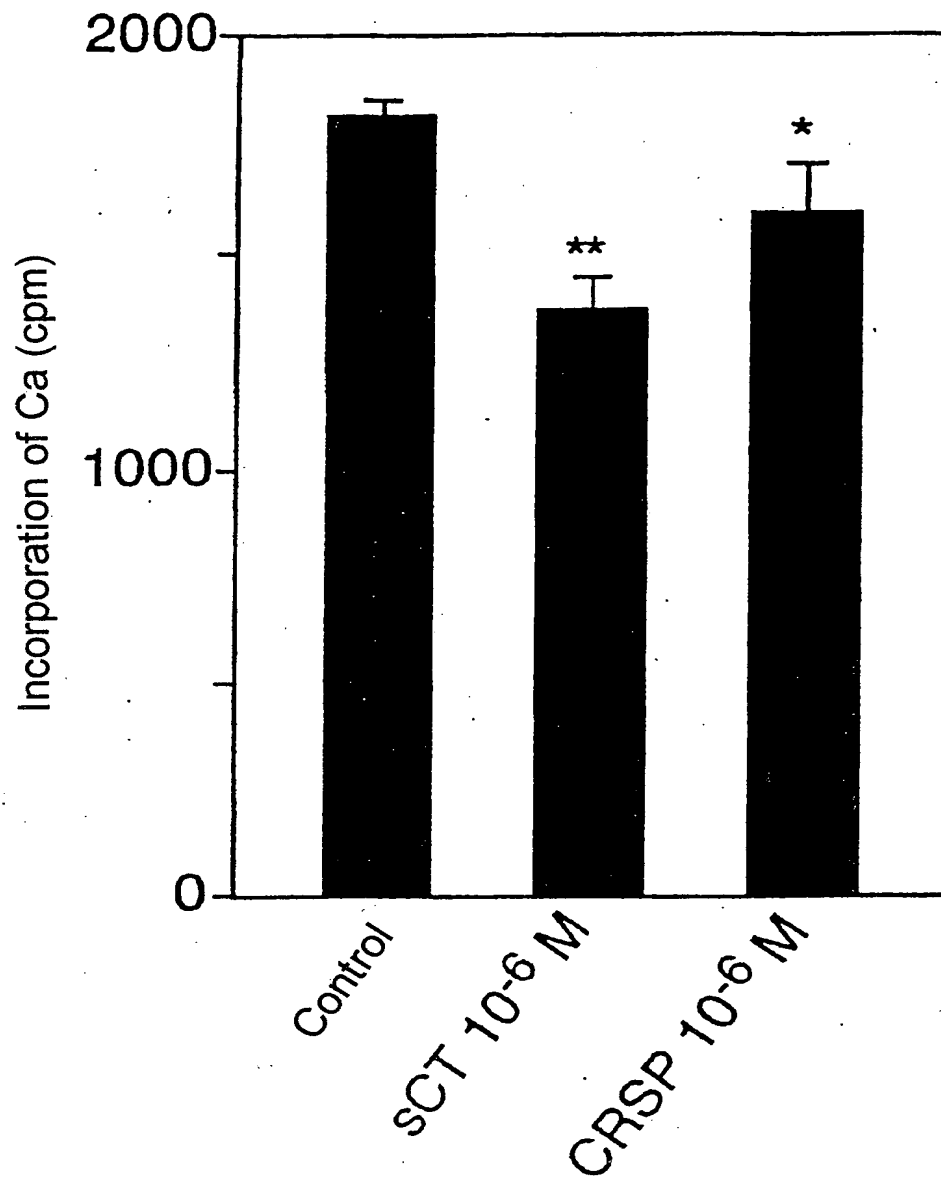


Fig. 8

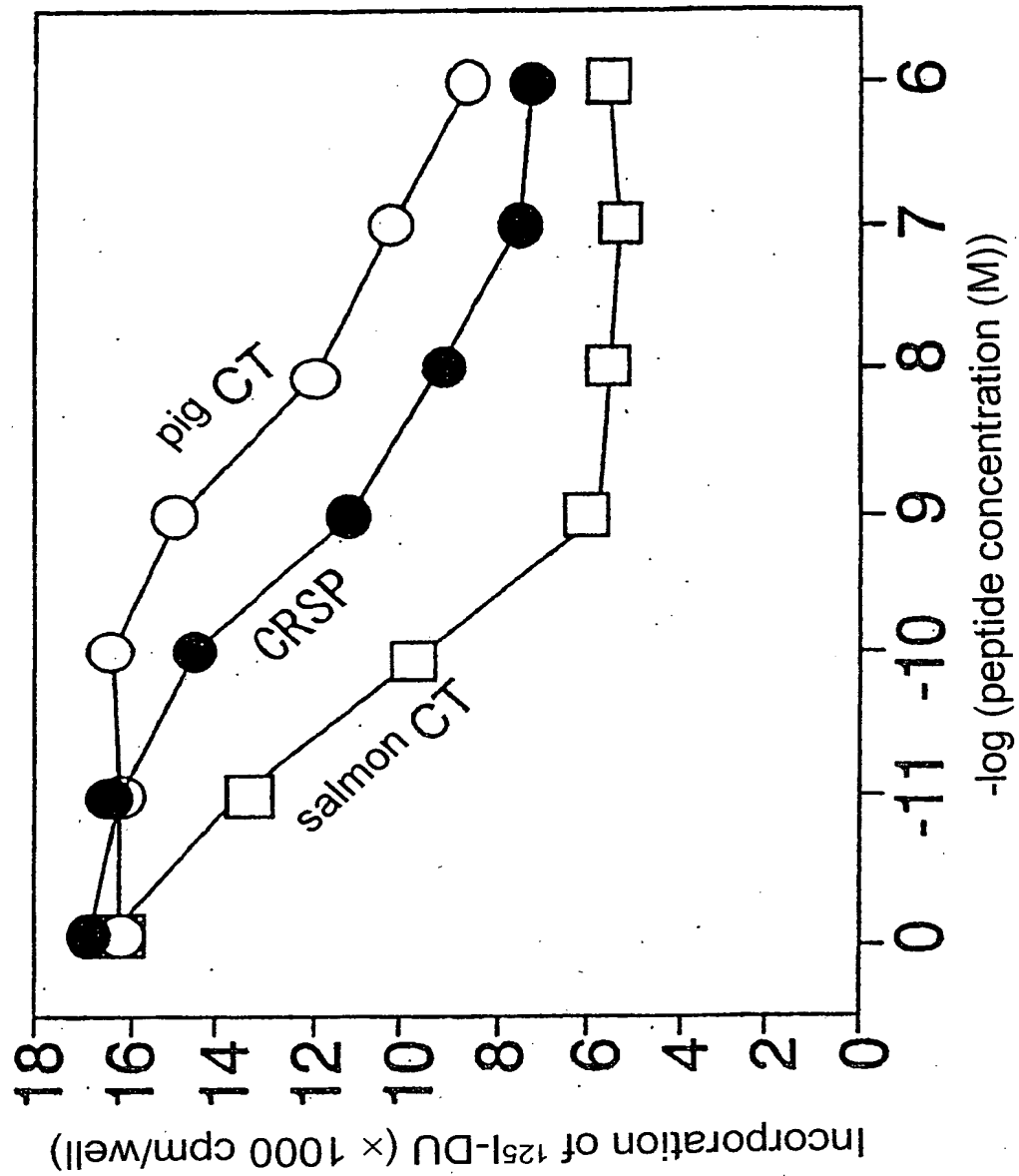




Fig. 9

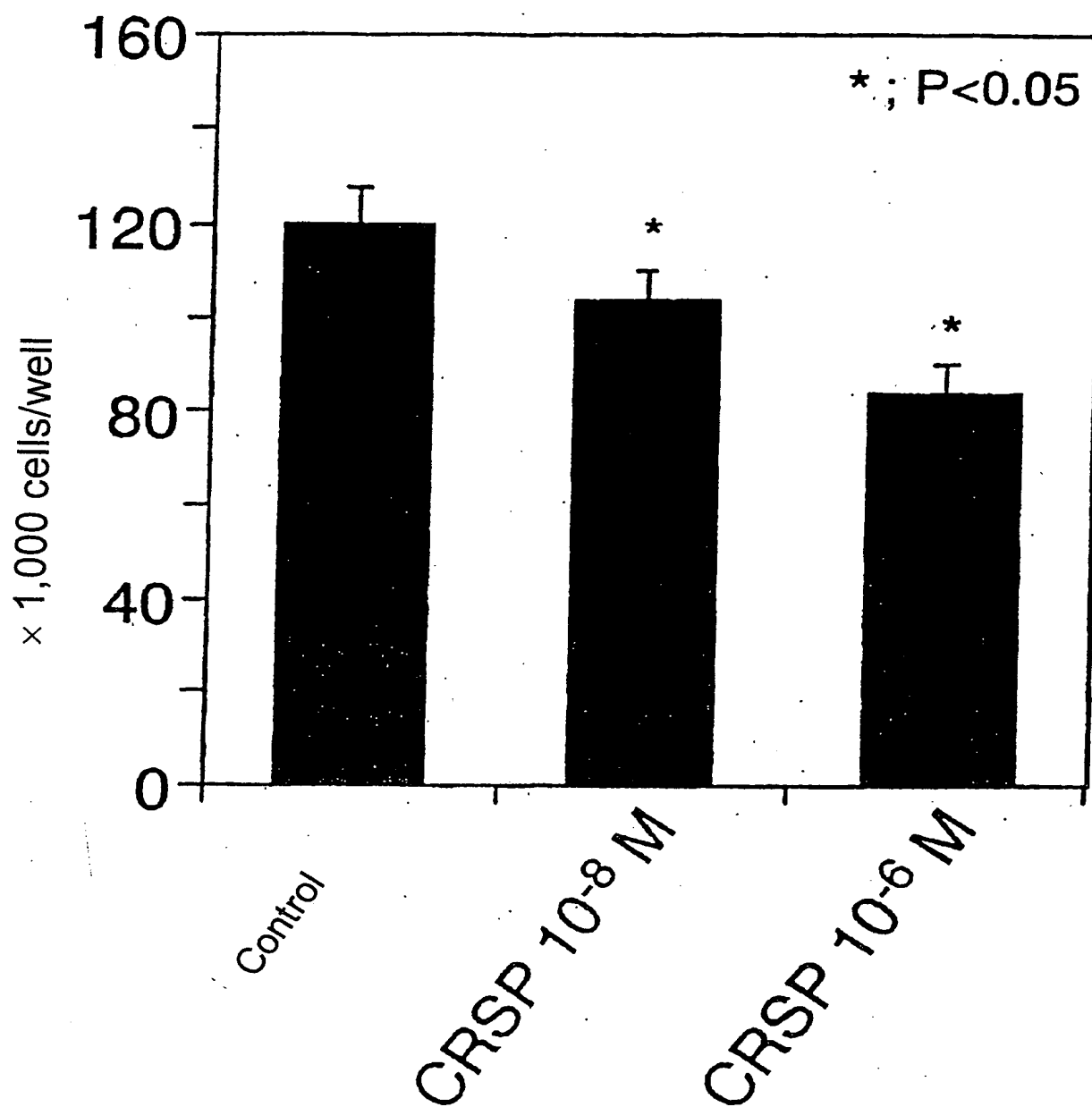


Fig. 10

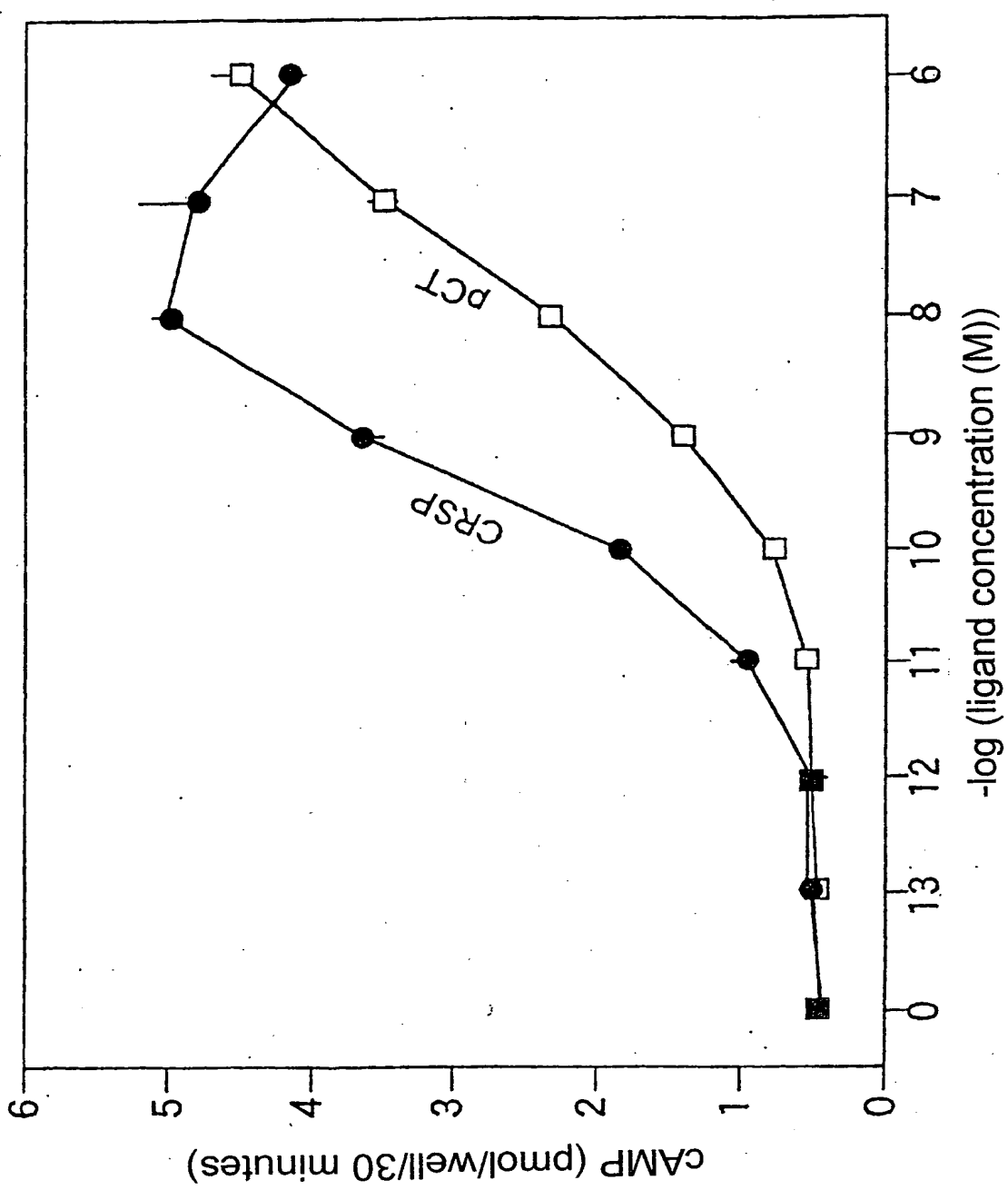


Fig. 11

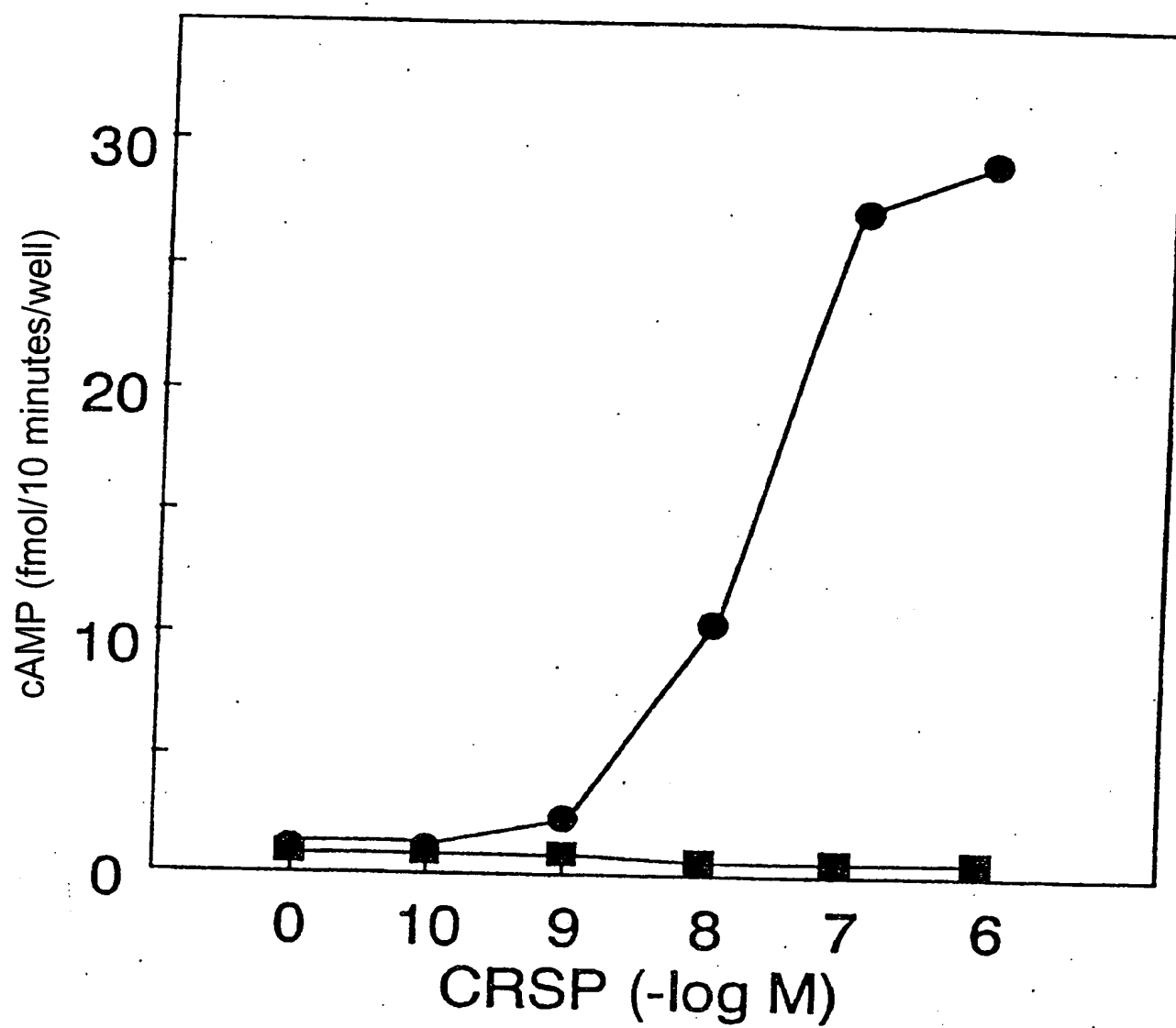


Fig. 12

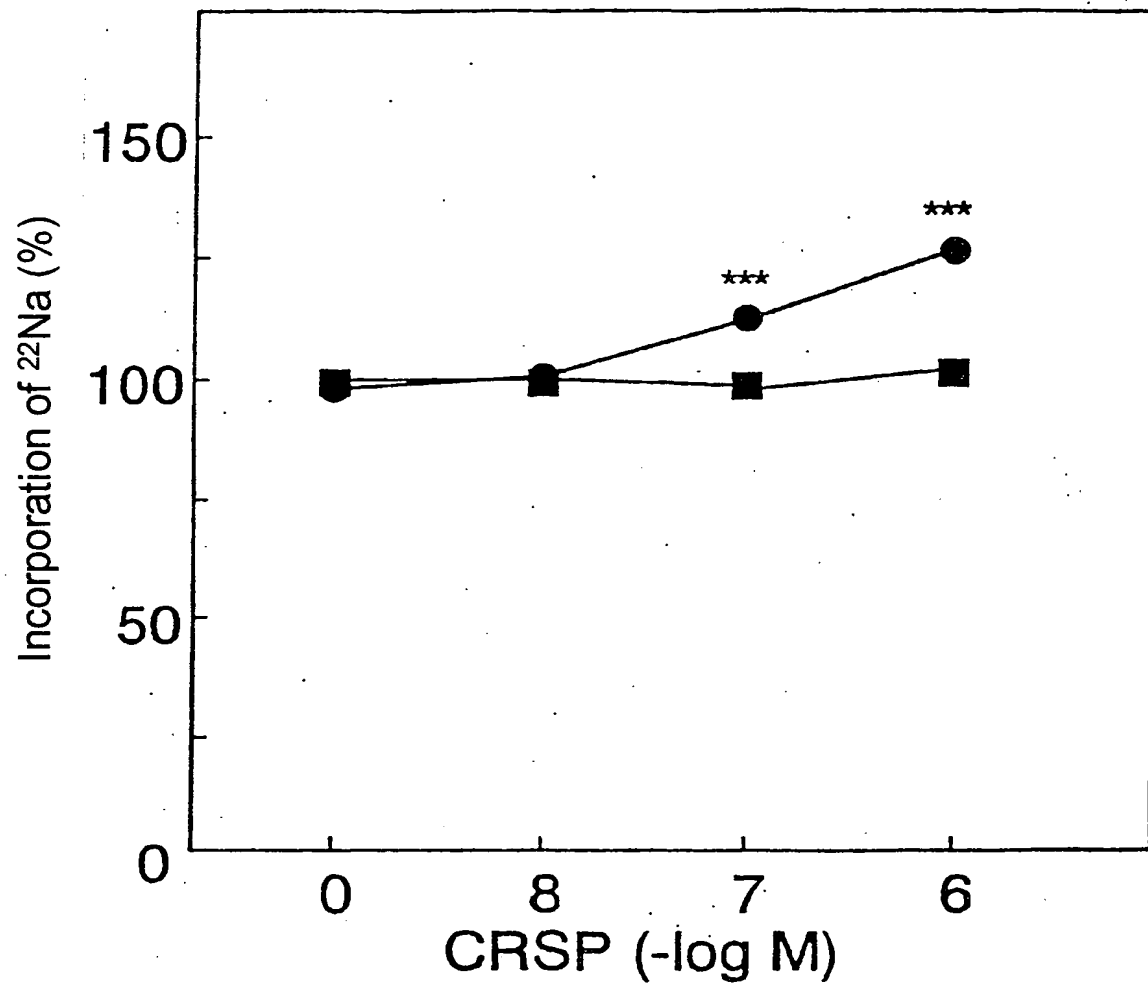


Fig. 13

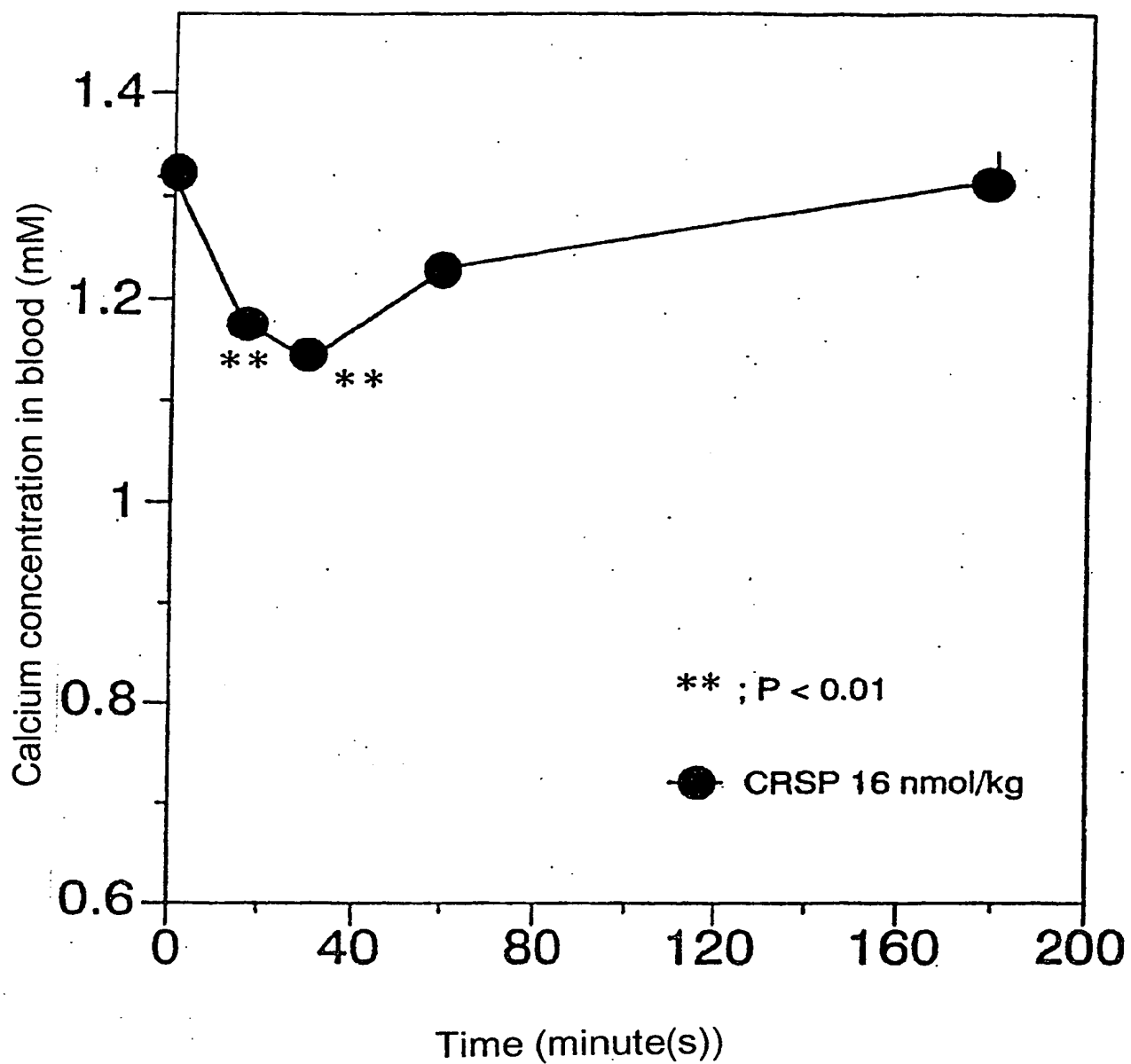


Fig. 14

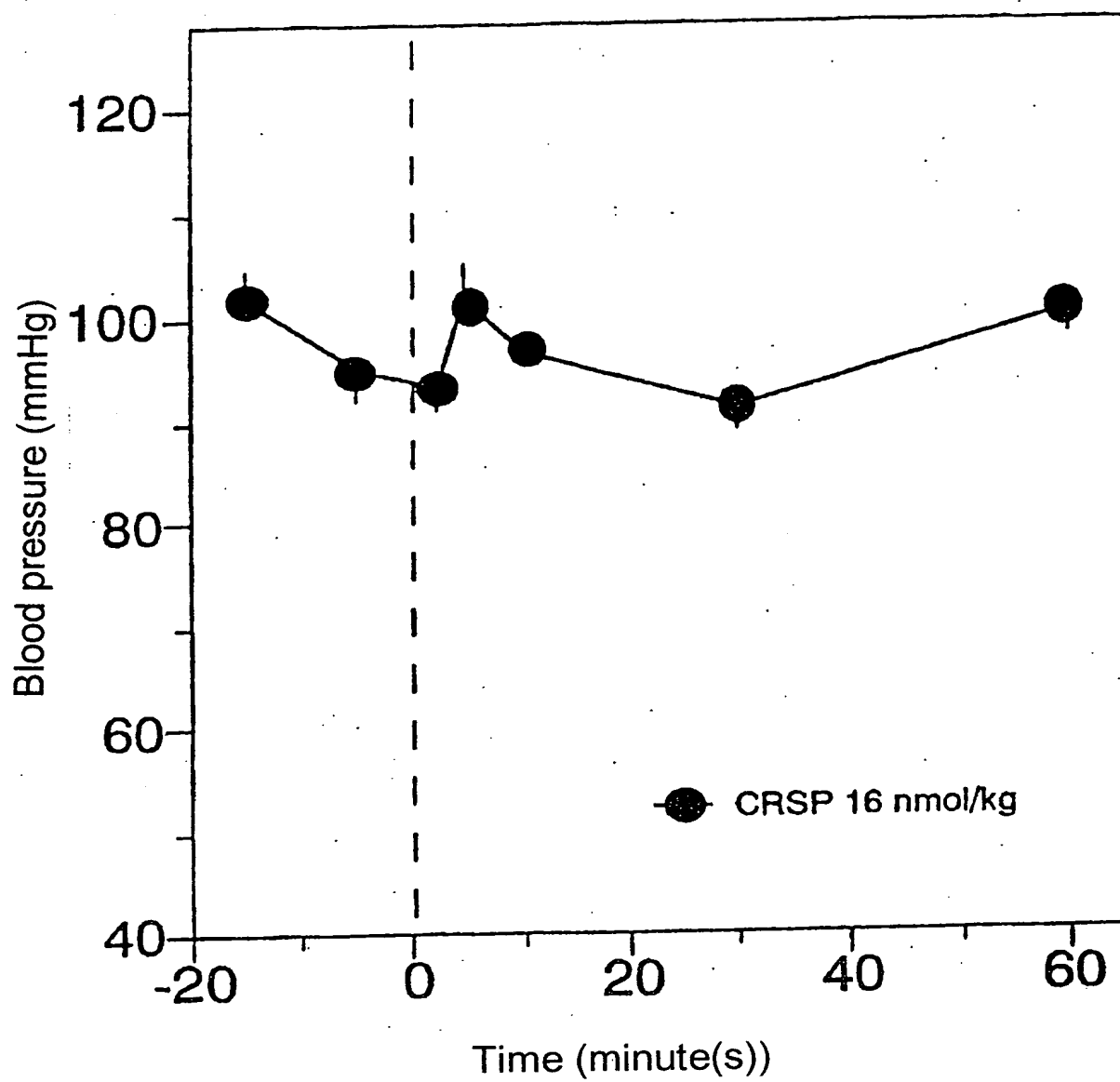


Fig. 15

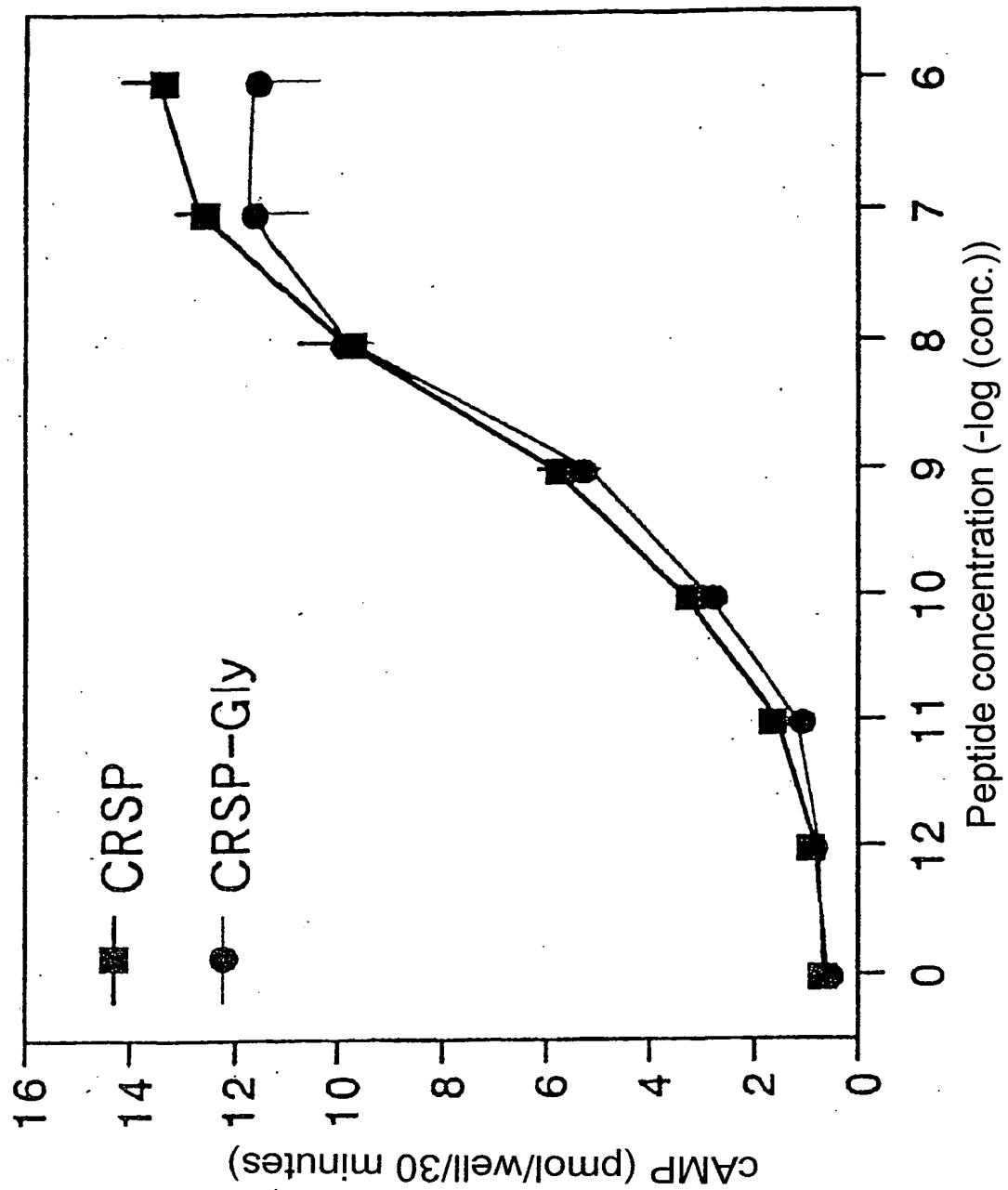
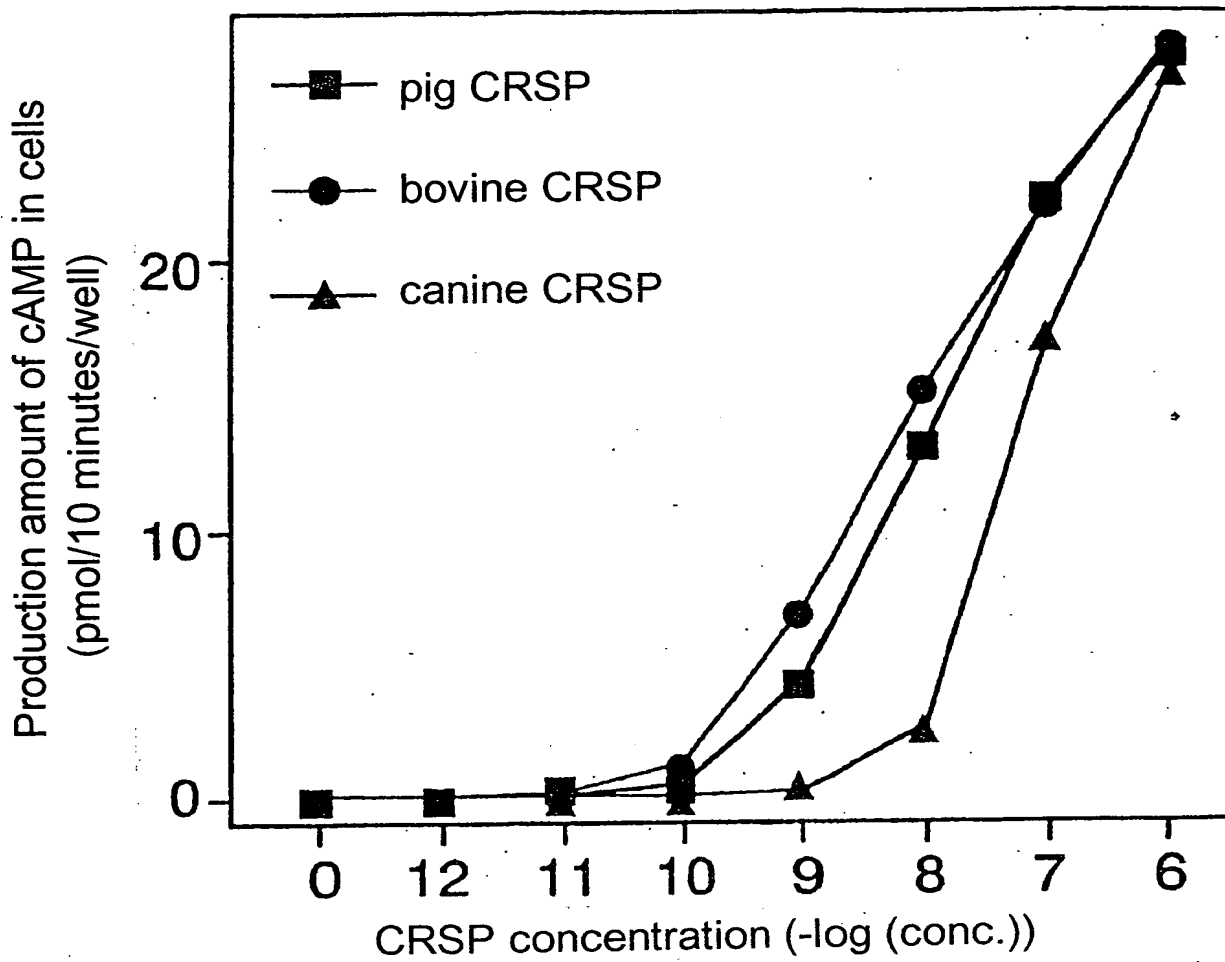


Fig. 16





## 第 17 図

CTCGAGGATCCTGCCTCTTGTTTCCCACAAATCCTGCCTTCCTGTGCTTGATTCCAGCTG	60
CCTGAATCAGACCCCCTGCTTGGGCACAGAATCATCAACCTGCTGCGCATTAACTCCCA	120
AACCGCACTTGGACATGGTAGTCTTAGGGGACCGGGGATGCCTTGTAATGCTGGACTCTG	180
CTCTACAAAGATCACATAGCTGGGGATGGAGAGGGATGTGAGCCTGCGAAACCGAACAGG	240
TAAAGTTTACCATGACGTCAAACGTCTTAAATTCCTGCTCACTTTGCGTGTGTTTTTC	300
GTTGGTGCCCAACCTCCCCACCCCTCCACCCCCGCCATCAATGACCTCAATGCAA	360
ATACAAGTGGGGTGGTCTGTTGGATGCTCCAGGTTCTGGACGCAAGTAGTGACACAATC	420
CTGGGGCTCAGGATCTTTCCTCTCATTGGTTGCCTGGAGCTCTGGGACCACCCAGATTTC	480
AGAGCGGCGGGAATAAGAGCAGCTGCTGGTGCGGGAAGGGTTAGAGGCCTACCCACCT	540
CAAGTGTCTCTGCCGCTTCTTCCACAGTGCCATCGCCTGACGCCAACGCTGCTGCCTCTG	600
CTCCCTCCTCTGCTCCAGTCCACCTGGTTCCTGCTGCCCCGTAAGCCCGGAGATTCTCTGC	660
TAAGCTGTGGTTCTGTTTCTCTCTCCCTCTCCTCCCTTCCCTCTCTCTCCATTGGATTTT	720
CTTAGCTGATCTCTTTTCCCGTCTCAAAGTTCCTGTCCACTTCTCTCTGGGTCTCTTCAT	780
CCTGTAATATGCCTTACTGCGCAATTCATTCTAGGCTCCTTTCACAGGTAACCTCGATG	840
GTCTCAGTTTCGGGGATTCCCTGCTCTACTCTTCCCTGAGCTGAGCTGGGCTCCAGTCTTGT	900
CCCCGCAGCAGACGTGCTTAGGTCCGTGTTGGGATTTTGGAGCTCTCCAGGCCTTCAGG	960
GAGAGGAGGATGCAGGAATAGCTTTGAGCAGAAGAACTTTCATGGATCCCATCTCCTCT	1020
TACCTACAAGGATCGCTGGAAATGGGGTCGGGACCTGGGACAGTGCAAATGGGTGGCAA	1080
TAGGTGCAATGACTGAGGGGAAAGTAGCTATTAACGCAAGCCCCAGTTGAAGGTTCTGG	1140
GAACTCCCCCTCCCGCACCGCCACCCCATTTAATCTTGGGTCCCAATTTAAGGCTGTACC	1200
AGCTTGTTTCTTACAGGGTGCTCTTTGCCAGAGTATGGAGCAGCTGGACAGTAAAATTTG	1260
GTTCTTCAGTTTCTCAGGGATTCCAACCTGCAGAGATATGTCTCCCAACTCCCCTTCCCC	1320
CCAGCCAGGTATAAGCAAAAATCAGGCATCAGGAGAGATGCTGATGGGTTGCACTATGGG	1380
AAAAGCTGTGGTGACAGGTACTGCGAGTCTGTCTCCAGGAGTCCCGGCCAACAGGTTGA	1440
AGGTGAGAGTGTGGGTGTGCTGGGCAGGGGGCTATGGACGGAGACCTCCTCACCCAGTTG	1500
TCCTGCTAGGCTTCTTTGCTAAACCAACATGTTGCAAGGCTCACTGGATCTTCCAGCAGT	1560
CCACTTGGCTGAGGAGGAAATGATGGTGAAAGGAAAGACACGAGCAGCCTGAAGCCAGG	1620
AAGCCAGGGAGTTGGAGGCAGAGGCAGGAGCAGAGCCCAGGTCTGTGGGCTCAATGAACT	1680
TGGAAGTGTACAGGTGGTGACATTGTTCTTCCCTTGCAAGGGGCACCATGGGCTTCTG	1740
MetGlyPheTr	
GAAATTTCCGCCCTTCCTGGTTCTCAGCATCCTGGTCCTGTACCAGGCAGGCATGTTCCA	1800
pLysPheProProPheLeuValLeuSerIleLeuValLeuTyrGlnAlaGlyMetPheHi	
CACAGCACCAATGAGGTAAGACAGCCCTGCCAACAAGCACACTCACTTGATGAGAATGTA	1860
sThrAlaProMetAr	
ATATAAACGTGTATATAAATTTATTATAAGGTGGCTCTGTAGAACAATGGATAGTGCCTT	1920
GCGCTCCTATAAGTTTATCATAAGCTTTATGTGTACACAAAGTTTGTAATAGACATAAG	1980
ATATACAGTACTCATGATTGTAAATTTTATATAACTTATCAAACCTCACAGCATGCTTTT	2040
TTGTTTTTCATCAAATATTTGTACCTTTAGCACACGTATATGCTCATATTACCATAATTTA	2100
AGAAATGGATTGTATCCAATTTGCCAAATACTTTGCTAGTAAATTTGTTATTAATCTGA	2160
TATGGGATCTACATCTCATTTTTTCACCTTCATTCAAACCTGCATTAAGCTAAAATTATT	2220
TTCCCATTCAAACTATCAGAAACCAGGCAACCTGGCTGTTTATCCTGGGGAGGGGCAGGC	2280
AGGAGATCAGAACCTGTTTTTAGGCTTGCTTCCCTCCTTAGGTCTGCCTTTGGGAGCCC	2340
gSerAlaPheGlySerPr	

Fig. 17

(continued)

<u>TTTTGATCCTGCTACCCTCTCTGAGGAGGAATCACGCCTCCTTTTGGCTGCAATGGTGAA</u>	2400
<i>oPheAspProAlaThrLeuSerGluGluGluSerArgLeuLeuLeuAlaAlaMetValAs</i>	
<u>TGACTATGAGCAGATGAAGGCGGTGAGATGCAGAAGCAGAGGGCACAGGGCTCCGGGTA</u>	2460
<i>nAspTyrGluGlnMetLysAlaArgGluMetGlnLysGlnArgAlaGlnGlySerGl</i>	
<u>AGGTTCCCTGCCCCAAGGACAACAGGGCATCCCTTTCTTCTCTGCTCAGGCCCAGGAAGG</u>	2520
<u>CATATTTTAAAGTCACTTTTGAGTTTTCTGACCCCCCTGGACATGTCTGTGGGATGATTA</u>	2580
<u>TGGCATTTCCTGACGGCCTAGGATTTTCTGCTGTGATGACCTTTTCTAGCAGAAATAC</u>	2640
<u>TCAAGGTTCACTGGTCTCTCAAGGCAGTAGTCTTCCATGACGATTCTGTCTGACAGCAC</u>	2700
<u>CTGCACTCAACCTCTCACTGACGGGCCTTTTCTTTCTTTATCCCAAAATCAGCATCAGT</u>	2760
<i>yIleSer</i>	
<u>GTCCAGAAGAGATCCTGCAACACTGCCACCTGCATGACCCATCGGCTGGTGGGCTTGCTC</u>	2820
<i>ValGlnLysArgSerCysAsnThrAlaThrCysMetThrHisArgLeuValGlyLeuLeu</i>	
<u>AGCAGATCTGGGAGCATGGTGAGGAGCAACCTGTTGCCCCACCAAGATGGGCTTCAAAGTC</u>	2880
<i>SerArgSerGlySerMetValArgSerAsnLeuLeuProThrLysMetGlyPheLysVal</i>	
<u>TTTGGTGGGCGCCGCAGGAACCTTTTGATCTGAGCAGTGGGATGATTCCAGGAGGAAGGT</u>	2940
<i>PheGlyGlyArgArgArgAsnPheTrpIle***</i>	
<u>GACTGCCCTTTTTGTACCTTCGGGTGGGAGGACAGAGGACTGGGTATTGCAGGGGTGCAT</u>	3000
<u>TCCACACCCTAACCCTCTGTGAGCGCATGGGGGTAAAACCTCCACATGGCAAGGTGCCCA</u>	3060
<u>CACCAGTGTCTGGAGAAAGGACTGATAATCCCTATAACTGAAACATTGGGCTCTTTCTCT</u>	3120
<u>CTGTTTCTCCAGTCTCTCCCTGTGACACTGACATCATCTGCCAGGAAATATAGACCCTGT</u>	3180
<u>TTACTTAAACACTGTTCCCTGGGTATTAATTGGGGTCCAGCTCTAGCATTAGAATTTGA</u>	3240
<u>AAGGTAATGACCCTACCCTTTTGGAGCATACTTACAATGTTATGAACTTGAGCATAGA</u>	3300
<u>CTCGGATTCAAATACTGTGTCTGTCTTCCACTAACTGTGACCATAGGCAAGTATGCCTCT</u>	3360
<u>GAGCCTCAGCTTCTCCTTGTAACCTGAAGGCAACAATAGTATCCTCAATATAAAAAATTAA</u>	3420
<u>TTAGTATAACATATGACAAGAGCCTGTAACTAAGAATTAATAACATTCTGTACTTTTT</u>	3480
<u>TCCCTCCTAGGTTACTATGACTCTGAACTCTACTTCGTTTAATTTACAATGAAAGCAACC</u>	3540
<u>TACTAAAAAATAGCATGGAAGACATCCATGTATGCATGCTTCTGGAAACTGAAAACACTC</u>	3600
<u>TTTTCCTTGAAATAAACTAAACTAAATGCAAAATAAAATCAATGCATCAATGCAGTTAC</u>	3660
<u>CTTGTGTGCATCTTTTGTGTATATGATTCTATAATATGATGCATGTCTCATTAGGTTTAA</u>	3720
<u>TGGTAGCAAATCTGGCCCCCTGTCAGCCAACCTGTTGGTGGGGCAGCTCTGCTAAACCTC</u>	3780
<u>AGGGTCACATGAATTC</u>	3796

Fig. 18

GGATCCACTAGTTCTAGATAAAATGGACAAATACCTAGAAACAGAAGACCTACCAAGATG 60  
GAAGGATGAAGAAATAGAAAATTCAAATACACCTATGACTAGGAAGGAGAATGAAGCATT 120  
AATCCAAAATCTTCCAACAAAGAAAAGCCCTGGATACGATGGCCTCATTGGTGAATAGTA 180  
CCAGACATTTAAAGAAAACGAATACCAATCCTTGTCAAACCTTTCCAAAAACCTGAAGAG 240  
AAAGGACACACCCTAACCTATTCTATGAGGCAGGCCAACATTACTCTGATACCAAAGATG 300  
GAGAAAGATTCTGCAAGGAGAAAACCCCTACAGACAAAATCCTTTATGACATGGATGTGG 360  
AAACCCCTCAACAGTATGCTAGGGAATTGAATTCAGAAGCGTATTTAAAAGGATCCTACAAC 420  
ATGACCAAGTGGGATGAATTTCTGGAATGCAAGGATGATTCAAAATATGAAAATTGATCA 480  
AAGTGTTATATCACAATAATGGAATGTAGGGAAAAACACACCTGATTATTTCCACTGATA 540  
CAGAAAATTATTTAGTAAAATTCAATACCTTTTCAGGATTAAAAACAAAACTAGGTATA 600  
GAAGGAGACTGCCTCAGCACAATAACAATATATGAAAAACCAACACCAACACCATAAT 660  
CCAGGGTGGAAAACCTGAAAGCTTTTCCCCTAAGATCTGGAAGAAAATGGAAAAAATTTT 720  
TAAGAATTTTCAGACAGATTTGGGTCTCTGGTACACTCTGAGAAATCATCTTTTAGAATT 780  
TTTTTTTTTTTAAAAATAAGCACAGAATTTTCATTTAAAAGAAGGGAAATAACATAGCCTT 840  
CAGAGTTTATCAGGAGGTGTAATTTTTTTTTTCCACACTAGATTGTGGCTACCTGATGCTA 900  
ATTTTGAGGTTTAAACATAATGAAATAAGATTGTACAGCCAAGTGCCAGCTAGTCATGGA 960  
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CAATACAAGTAATCGGTACTTGCTGAAGGTCTAAAATTTTCAGGTGCACTTGGTAAATCAG 1080  
GGATGGGCGCAGAGGAGACTGGTTCTGTAACCTCAGACTAGTGAACCCTAGAATTTAGAAA 1140  
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GCTGTAGTTAGAGCCCTCTCATAGCAGGGAGACTGCCTTGGTGAATCTGCCAGAGGAAAT 1260  
GAATTTCCATTACATTCATTCAACAAACATTGGGCGAGTGCCACCTCATGTGCAAAACA 1320  
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CTTAGCCATAGTGCAGCCACCTTTGCATTGATCAAACTGTGGTTCTTCCAATGAAAAAA 1740  
GACATCCCCAGACACATACTTACAAATGATTTCAGAAGATTGATAGGTCGGAAATCTC 1800  
AGGTTTTTGGATTTTATTTGCAAAAGCGTTTTTGGCGCTGAGTTTTAAACTTTTTTTTTT 1860  
TTTTTTTTTTTTTGATTTTTTCACTTCTAGGGCGGCTTCGGCGGCATATGGAAATTCCCAG 1920

## 第 18 図 続き

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 GTGCACCCAATTTTTGCTTGTAGTAGAAACCAGGATTTACGGAGCCCAGCAGTCCGCCA 2340  
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 CCAGTTTTTCCGTTCCCTTGGTCTCCCGATCCGTTGTCTATCCTGAGGAGAGCGAGATGC 2460  
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 GGGTATCTTGTAATGAGATGTTCCGAGTCCAGAGAGCACAAACCGGCAAGGGGAACAGA 2580  
 TGTGCCGCGAGGCAGGTGTGCGGAAAGATATAGAGAAGGCTCAGGTTCGGACCTGTGGCT 2640  
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 CTCCCACCCCCGCCATCAATGACCTCAATGCAAATACAAGTGGGGTGGTCCCTGTTGGATG 3720  
 CTCCAGGTTCTGGACGCAAGTAGTGACACAATCCTGGGGCTCAGGATCTTTCCTCTCATT 3780  
 GGTGCTGAGCTCTGGGACCACCCAGATTCAGAGCGGCGGAATAAGAGCAGCTGCT 3840

Fig. 19

GGTGCGGGGAAGGGTTAGAGGCACTACCCACCTCAAGTGTCTCTGCCGCTTCTTCCACAG 3900  
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 TCTCCTCCCTTCCCTCTCTCTCCATTGGATTTTCTTAGCTGATCTCTTTTCCCGTCTCAA 4080  
 AGTTCTGTCCACTTCTCTCTGGGTCTCTTCATCCTGTAATATGCCTTACTGCGCAATTC 4140  
 ATTCTAGGCTCCTTTTACAGGTAACCTCTGGATGGTCTCAGTTCGGGGATTCCCTGCTCTA 4200  
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 GTTGGGATTTTGGAGCTCTCCAGGCACTTCAGGGAGAGGAGGATGCAGGAATAGCTTTGA 4320  
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 CTATTAAACGCAAGCCCCAGTTGAAGGTTCTGGGAACTCCCCCTCCCGCACC GCCACCCC 4500  
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 CCAGAGTATGGAGCAGCTGGACAGTAAAATTTGGTTCTTCAGTTTCTCAGGGATTCCAAC 4620  
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 ATCAGGAGAGATGTCTGATGGGTGCACTATGGGAAAAGCTGTGGTGACAGGTACTGTGAG 4740  
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*MetGlyPheTrpLysPheProProPheLeuValLeuSe*

CATCCTGGTCCTGTACCAGGCAGGCATGTTCCACACAGCACCCGTGAGGTAAGACAGCAC 5160  
*rIleLeuValLeuTyrGlnAlaGlyMetPheHisThrAlaProValAr*

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 GCATGTTGGGCTTGCTTTCCCTTCCCAGATTGCCCTTTGGAGAGCAGCTTTGATTCTGCCA 5940

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## 第 19 図 続き

TGAAGGCCACTGTGCTGGAGCAGGAGTCAGAGGACTTCAGGTCAGTCTTTGCACCCCTCC 6060  
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 TGGGAGCGTGGCTAAGAACAACCTTCATGCCACCAATGTGGACTCCAAAATCTTGGGCTG 6600  
 rGlySerValAlaLysAsnAsnPheMetProThrAsnValAspSerLysIleLeuGly\*\*  
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 \*  
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 TCTTCCACTAACTATAACAACCATGGGCCAGACCCCTCTCTGAACCTCAGTTCTACATGAAA 7260  
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 TAGGTCAACCAAGGAACTGAACCTATTTCTTTTAATCTGCAATGAAAGCAATTTATTGTA 7440  
 AAAATAGCATGGAAAACACACATATATGCATGCTTCTTGCTTGAAATACAGCTTTTAGCT 7500  
 TGAAATAAACTAAACTAAATGCAGAATAAAATCATTCAGCTACCTGATATGTATCATT 7560  
 TTAATATTTGATTCTGTATTCTATAAGTATGACTCATGTCTCGCTGGCTTATCTGGTAGC 7620  
 AAATCTGGACCCTGTCAGCCAACCTGTGGTGGTGGCAGCTCTGCTAAACCTC 7673

Fig. 20

CTCAAGTGTCTCTGCCGCTTCTTCCACAGTGCCATCGCCTGACGCCAACGCTGCTGCCTC	-52
TGCTCCCTCCTCTGCTCCAGTCCACCTGGTTCCTGCTGCCCGAGGGGCACCATGGGCTTC	9
	M G F 3
TGGAAATTTCCGCCCTTCCTGGTTCTCAGCATCCTGGTCCTGTACCAGGCAGGCATGTTT	69
W K F P P F L V L S I L V L Y Q A G M F	23
CACACAGCACCCGTGAGATTGCCTTTGGAGAGCAGCTTTGATTCTGCCACTCTCACAGAG	129
H T A P V R L P L E S S F D S A T L T E	43
GAGGAAGTGTCCCTTCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT	189
E E V S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGTCAGAGGACTTCAGCATCACTGCCCAGGAGAAATCCTGCAACACT	249
V L E Q E S E D F S I T A Q E K <u>S C N T</u>	83
GCTAGCTGTGTGACCCACAAGATGACAGGCTGGCTGAGCAGATCTGGGAGCGTGGCTAAG	309
<u>A S C V T H K M T G W L S R S G S V A K</u>	103
AACAAC TTCATGCCACCAATGTGGACTCCAAAATCTTGGGCTGACGCCGCAGAGAGCCT	369
<u>N N F M P T N V D S K I L</u> <span style="background-color: #cccccc;">G</span>	117
CAGGCCTGAGCTGTGAAATGACTCCACAAAGAAGGTCACCAAGGAACTGAACTCTATTTT	429
TTTTAATCTGCAATGAAAGCAATTTATTTGAAAAATAGCATGGAAAACACACATATATGC	489
ATGCTTCTTGCTTGAAATACAGCTTTTAGCTTGAAATAAACTAAACTAAATGCAGAATA	549
AAATCATTGCAGCTACCTGAAAAAAAAA	579

Fig. 21

GCCCAGCTTACGTCTCCTTTCTCCGCCAGTGCCATCACCTGCCACCAGCGCGGTTGTTGC -52  
 TTCTCCCACCTTGGGCTCCAAGCTACCTGGTTCTGCATCCAGAGGGGCACCATGGGCTTC 9  
 M G F 3


TGAAGTTCCCCCCTTCCTGATCCTCAGCATCCTGGTCCTGTACCAAGCAGGAATGCTC 69  
 W K F P P F L I L S I L V L Y Q A G M L 23

CATGCCGCGCCATTCAGGATGGCTTTGGGAAGCAGCTTTGATTCTGCCACACTCACGGAA 129  
 H A A P F R M A L G S S F D S A T L T E 43

GAGGAAATGTCCCTCCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT 189  
 E E M S L L L V A M V K D Y V Q M K A T 63

GTGCTGGAGCAGGAGACAGAGGACTTCAGCATCACCACCCAGGAGAGATCCTGCAACACT 249  
 V L E Q E T E D F S I T T Q E R S C N T 83

GCCATCTGTGTGACCCACAAGATGGCAGGCTGGCTGAGCAGATCTGGGAGCGTGGTTAAG 309  
A I C V T H K M A G W L S R S G S V V K 103

AACAACTTCATGCCCATCAACATGGGCTCCAAAGTCTTGGGCCCGCGCCGCAGACAGCCT 369  
N N F M P I N M G S K V L  R R R R Q P 123

CAGGCCTGAGCTGTGAAATGACTCTAAAAAGAAGTTGAACTCAAGTTGCTTTCACTGCAA 429  
 Q A \* 125

AGTTGCTTTCCCTGCAAATTAAGAAGCAATTTGAAAAATAGCATGGAAGACACACATA 489  
 TATGCATGCTTCTTGCTTGAAATACAACCTTTTGCTTGAAACAACTAAACCTAAATGCA 549  
 GAATAAAATCATTGCAGTTACCTGA 574



Fig. 22


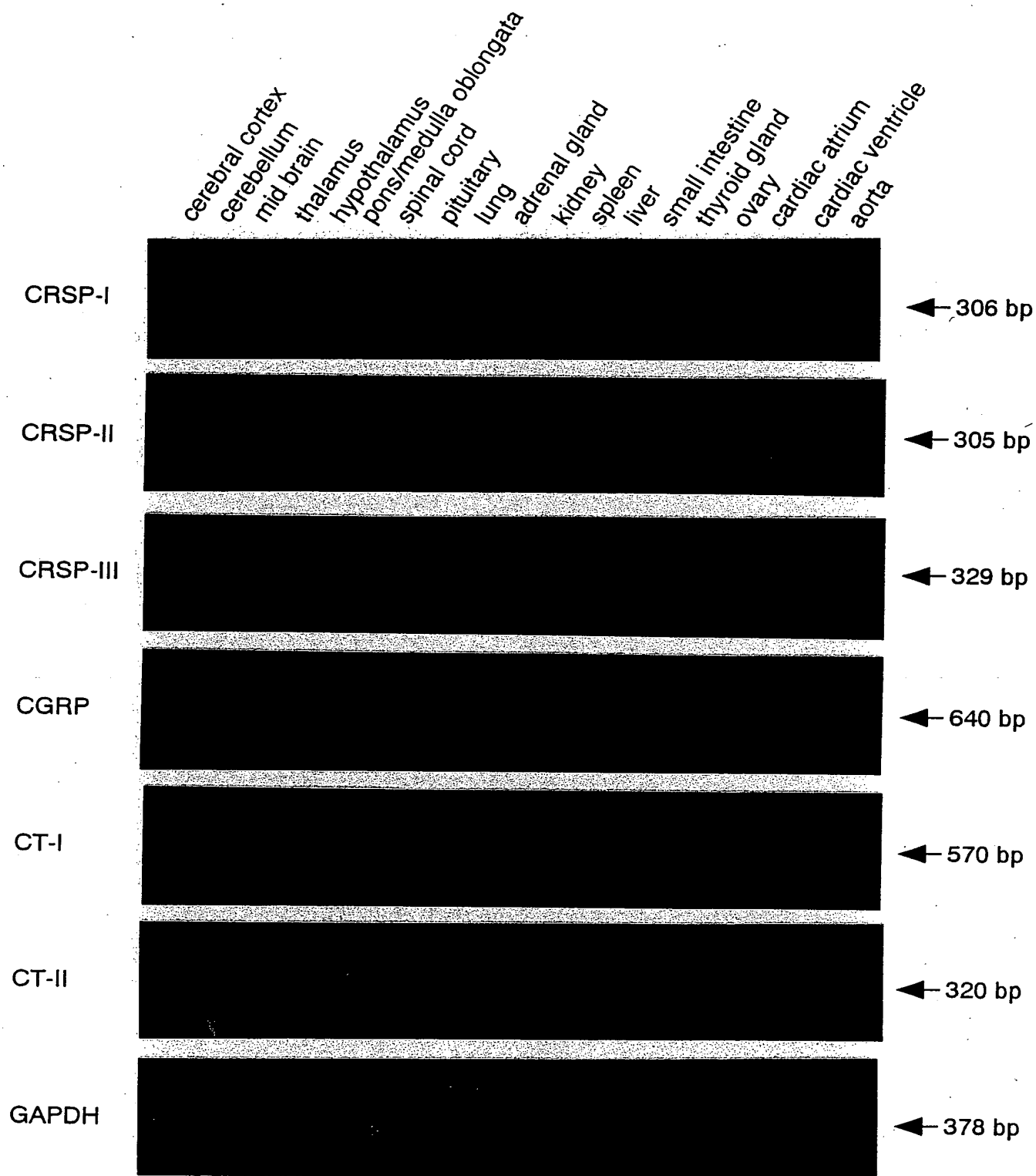
CCCCAGCTTACGTCTCCTTTCTCCGCCAGTGCCATCACCTGCCACCAGCGCGGTTGTTGC	-52
TTCTCCCACCTTGGGCTCCAAGCTACCTGGTTCCTGCATCCAGAGGGGCACCATGGGCTTC	9
	M G F 3
TGGAAGTTCCCCCCTTCCTGATCCTCAGCATCCTGGTCCTGTACCAAGCAGGAATGCTC	69
W K F P P F L I L S I L V L Y Q A G M L	23
CATGCCGCGCCATTCAGGATGGCTTTGGGAAGCAGCTTTGATTCTGCCACACTCACGGAA	129
H A A P F R M A L G S S F D S A T L T E	43
GAGGAAATGTCCCTCCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT	189
E E M S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGACAGAGGACTTCAGCCTGGACAGCTCCAGAGCTAAGCAGTGCAAT	249
V L E Q E T E D F S L D S S R A K <u>Q C N</u>	83
AATCTGAGTACCTGTGTGCTGGGAACATATACATGGGACGTCAACAAGTTTTATGCATTC	309
<u>N L S T C V L G T Y T W D V N K F Y A F</u>	103
CCCTTAACTACAACCTGGGATTAGAGTATCTGGCAAGAAATGGGTCAGGGCCAGAGTCTCA	369
<u>P L T T T G I R V S</u>  K K W V R A R V S	123
GAGAAAGTCCATTATCCCTCAAGGCAGCATACCCTAAGGTGCTTAAGAAGGCCCCACCC	429
E K V H Y P S R Q H T L R C L R R P P P	143
CTCCTCCTTTCTAGTTCTCTCCTAGAATTTGCATGTGTTCTTCTCTGGTTGCTCTCTGA	489
L L L S S S S P R I C M C S S L V A L	162
GCTGCTATCAGCAGCTTTCCTTGTGGCCATGGATGTCTGGAATATCAGAGAGGAGGTGGG	549
GGTGGGGGCAGGCAGGCCAGAAGAAAATCACTCAGGAATAGATTAGGAGAGAATGGGCA	609
CCCCTGTGAGTGCCTGTGGATTTACAGCAGAGCTTCTCAGTCCTGCTTCTGAACATGCT	669
TTTCACTAGGGAATAAAAAGTAT	691

Fig. 23

SCNTASCVTHKMTGWLRSRGSVAKNNFMP-TNVDSKIL-NH<sub>2</sub> pCRSP-2  
 SCNTAICVTHKMAAGWLSRSGSVVKNNFMP-INMGSKVL-NH<sub>2</sub> pCRSP-3  
 SCNTATCMTHRLVGLLSRSGSMVRSNLLP-TKMGEKVFVFG-NH<sub>2</sub> pCRSP  
 SCNTATCVTHRLAGLLSRSGGMVKSNFVP-TDVGSEAF-NH<sub>2</sub> pCGRP  
 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAFPRSKI SPQGY-NH<sub>2</sub> pAM

CSNLSSTCVLSAYWRNLNNEHREFSGMGFGPETP-NH<sub>2</sub> pCT  
 PECNNLSSTCVLGTYTWDVNKEFYAFPLTTTGIRVS-NH<sub>2</sub> pCT-2

Fig. 24



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